



IFWO

RAW SEQUENCE LISTING

DATE: 09/10/2004

PATENT APPLICATION: US/10/719,695

TIME: 10:22:25

Input Set : A:\Isa01201.app

Output Set: N:\CRF4\09102004\J719695.raw

3 <110> APPLICANT: NG, LEONG
 5 <120> TITLE OF INVENTION: BODILY FLUID MARKERS OF TISSUE HYPOXIA
 7 <130> FILE REFERENCE: ISA-012.01
 9 <140> CURRENT APPLICATION NUMBER: 10/719,695
 10 <141> CURRENT FILING DATE: 2003-11-21
 12 <150> PRIOR APPLICATION NUMBER: GB 0322390.6
 13 <151> PRIOR FILING DATE: 2003-09-24
 15 <150> PRIOR APPLICATION NUMBER: GB 0227179.9
 16 <151> PRIOR FILING DATE: 2002-11-21
 18 <160> NUMBER OF SEQ ID NOS: 3
 20 <170> SOFTWARE: PatentIn Ver. 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 999
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
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 32 20 25 30
 34 Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met Lys Val Ala
 35 35 40 45
 37 Ile Val Lys Pro Gly Val Pro Met Glu Ile Val Leu Asn Lys Glu Ser
 38 50 55 60
 40 Arg Arg Lys Thr Pro Val Ile Val Thr Leu Lys Glu Asn Glu Arg Phe
 41 65 70 75 80
 43 Phe Gly Asp Ser Ala Ala Ser Met Ala Ile Lys Asn Pro Lys Ala Thr
 44 85 90 95
 46 Leu Arg Tyr Phe Gln His Leu Leu Gly Lys Gln Ala Asp Asn Pro His
 47 100 105 110
 49 Val Ala Leu Tyr Gln Ala Arg Phe Pro Glu His Glu Leu Thr Phe Asp
 50 115 120 125
 52 Pro Gln Arg Gln Thr Val His Phe Gln Ile Ser Ser Gln Leu Gln Phe
 53 130 135 140
 55 Ser Pro Glu Glu Val Leu Gly Met Val Leu Asn Tyr Ser Arg Ser Leu
 56 145 150 155 160
 58 Ala Glu Asp Phe Ala Glu Gln Pro Ile Lys Asp Ala Val Ile Thr Val
 59 165 170 175
 61 Pro Val Phe Phe Asn Gln Ala Glu Arg Arg Ala Val Leu Gln Ala Ala
 62 180 185 190
 64 Arg Met Ala Gly Leu Lys Val Leu Gln Leu Ile Asn Asp Asn Thr Ala
 65 195 200 205
 67 Thr Ala Leu Ser Tyr Gly Val Phe Arg Arg Lys Asp Ile Asn Thr Thr

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68      210      215      220
70 Ala Gln Asn Ile Met Phe Tyr Asp Met Gly Ser Gly Ser Thr Val Cys
71 225      230      235      240
73 Thr Ile Val Thr Tyr Gln Met Val Lys Thr Lys Glu Ala Gly Met Gln
74      245      250      255
76 Pro Gln Leu Gln Ile Arg Gly Val Gly Phe Asp Arg Thr Leu Gly Gly
77      260      265      270
79 Leu Glu Met Glu Leu Arg Leu Arg Glu Arg Leu Ala Gly Leu Phe Asn
80      275      280      285
82 Glu Gln Arg Lys Gly Gln Arg Ala Lys Asp Val Arg Glu Asn Pro Arg
83      290      295      300
85 Ala Met Ala Lys Leu Leu Arg Glu Ala Asn Arg Leu Lys Thr Val Leu
86 305      310      315      320
88 Ser Ala Asn Ala Asp His Met Ala Gln Ile Glu Gly Leu Met Asp Asp
89      325      330      335
91 Val Asp Phe Lys Ala Lys Val Thr Arg Val Glu Phe Glu Glu Leu Cys
92      340      345      350
94 Ala Asp Leu Phe Glu Arg Val Pro Gly Pro Val Gln Gln Ala Leu Gln
95      355      360      365
97 Ser Ala Glu Met Ser Leu Asp Glu Ile Glu Gln Val Ile Leu Val Gly
98      370      375      380
100 Gly Ala Thr Arg Val Pro Arg Val Gln Glu Val Leu Leu Lys Ala Val
101 385      390      395      400
103 Gly Lys Glu Glu Leu Gly Lys Asn Ile Asn Ala Asp Glu Ala Ala Ala
104      405      410      415
106 Met Gly Ala Val Tyr Gln Ala Ala Ala Leu Ser Lys Ala Phe Lys Val
107      420      425      430
109 Lys Pro Phe Val Val Arg Asp Ala Val Val Tyr Pro Ile Leu Val Glu
110      435      440      445
112 Phe Thr Arg Glu Val Glu Glu Glu Pro Gly Ile His Ser Leu Lys His
113      450      455      460
115 Asn Lys Arg Val Leu Phe Ser Arg Met Gly Pro Tyr Pro Gln Arg Lys
116 465      470      475      480
118 Val Ile Thr Phe Asn Arg Tyr Ser His Asp Phe Asn Phe His Ile Asn
119      485      490      495
121 Tyr Gly Asp Leu Gly Phe Leu Gly Pro Glu Asp Leu Arg Val Phe Gly
122      500      505      510
124 Ser Gln Asn Leu Thr Thr Val Lys Leu Lys Gly Val Gly Asp Ser Phe
125      515      520      525
127 Lys Lys Tyr Pro Asp Tyr Glu Ser Lys Gly Ile Lys Ala His Phe Asn
128      530      535      540
130 Leu Asp Glu Ser Gly Val Leu Ser Leu Asp Arg Val Glu Ser Val Phe
131 545      550      555      560
133 Glu Thr Leu Val Glu Asp Ser Ala Glu Glu Glu Ser Thr Leu Thr Lys
134      565      570      575
136 Leu Gly Asn Thr Ile Ser Ser Leu Phe Gly Gly Gly Thr Thr Pro Asp
137      580      585      590
139 Ala Lys Glu Asn Gly Thr Asp Thr Val Gln Glu Glu Glu Glu Ser Pro
140      595      600      605

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142 Ala Glu Gly Ser Lys Asp Glu Pro Gly Glu Gln Val Glu Leu Lys Glu
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145 Glu Ala Glu Ala Pro Val Glu Asp Gly Ser Gln Pro Pro Pro Pro Glu
146 625      630      635      640
148 Pro Lys Gly Asp Ala Thr Pro Glu Gly Glu Lys Ala Thr Glu Lys Glu
149      645      650      655
151 Asn Gly Asp Lys Ser Glu Ala Gln Lys Pro Ser Glu Lys Ala Glu Ala
152      660      665      670
154 Gly Pro Glu Gly Val Ala Pro Ala Pro Glu Gly Glu Lys Lys Gln Lys
155      675      680      685
157 Pro Ala Arg Lys Arg Arg Met Val Glu Glu Ile Gly Val Glu Leu Val
158      690      695      700
160 Val Leu Asp Leu Pro Asp Leu Pro Glu Asp Lys Leu Ala Gln Ser Val
161 705      710      715      720
163 Gln Lys Leu Gln Asp Leu Thr Leu Arg Asp Leu Glu Lys Gln Glu Arg
164      725      730      735
166 Glu Lys Ala Ala Asn Ser Leu Glu Ala Phe Ile Phe Glu Thr Gln Asp
167      740      745      750
169 Lys Leu Tyr Gln Pro Glu Tyr Gln Glu Val Ser Thr Glu Glu Gln Arg
170      755      760      765
172 Glu Glu Ile Ser Gly Lys Leu Ser Ala Ala Ser Thr Trp Leu Glu Asp
173      770      775      780
175 Glu Gly Val Gly Ala Thr Thr Val Met Leu Lys Glu Lys Leu Ala Glu
176 785      790      795      800
178 Leu Arg Lys Leu Cys Gln Gly Leu Phe Phe Arg Val Glu Glu Arg Lys
179      805      810      815
181 Lys Trp Pro Glu Arg Leu Ser Ala Leu Asp Asn Leu Leu Asn His Ser
182      820      825      830
184 Ser Met Phe Leu Lys Gly Ala Arg Leu Ile Pro Glu Met Asp Gln Ile
185      835      840      845
187 Phe Thr Glu Val Glu Met Thr Thr Leu Glu Lys Val Ile Asn Glu Thr
188      850      855      860
190 Trp Ala Trp Lys Asn Ala Thr Leu Ala Glu Gln Ala Lys Leu Pro Ala
191 865      870      875      880
193 Thr Glu Lys Pro Val Leu Leu Ser Lys Asp Ile Glu Ala Lys Met Met
194      885      890      895
196 Ala Leu Asp Arg Glu Val Gln Tyr Leu Leu Asn Lys Ala Lys Phe Thr
197      900      905      910
199 Lys Pro Arg Pro Arg Pro Lys Asp Lys Asn Gly Thr Arg Ala Glu Pro
200      915      920      925
202 Pro Leu Asn Ala Ser Ala Ser Asp Gln Gly Glu Lys Val Ile Pro Pro
203      930      935      940
205 Ala Gly Gln Thr Glu Asp Ala Glu Pro Ile Ser Glu Pro Glu Lys Val
206 945      950      955      960
208 Glu Thr Gly Ser Glu Pro Gly Asp Thr Glu Pro Leu Glu Leu Gly Gly
209      965      970      975
211 Pro Gly Ala Glu Pro Glu Gln Lys Glu Gln Ser Thr Gly Gln Lys Arg
212      980      985      990
214 Pro Leu Lys Asn Asp Glu Leu

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218 <210> SEQ ID NO: 2
219 <211> LENGTH: 13
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
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228 <210> SEQ ID NO: 3
229 <211> LENGTH: 14
230 <212> TYPE: PRT
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
235 peptide
237 <400> SEQUENCE: 3
238 Cys Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met
239 1 5 10

VERIFICATION SUMMARY

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